

Table 1

3. Permutation table

Protein	Seq Possible deletions	Insertion positions (Ω) of the inserts (AS position/Seq ID)
ID (AS position/AS number)	bridge compos. 1, 2, 3 native bridge compos. 1 epitopes	(seq ID 1-3) (seq ID 4) (seq ID 5-36)

Table 2

2. Amino acid sequences

Seq ID	Amino acid sequence	Seq ID	Amino acid sequence
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Legend : X \equiv D or E

"-" \equiv an arbitrary amino acid

Fig. 1

1. Amino acid sequences (single letter amino acid code)

Legend: [or] \equiv beginning or end of a possible deletion
 +A/B+ \equiv possible insertion positions of an AA sequence with the Seq ID A
 and/or B

Fig. 3

3. Permutationstabelle

Protein	Seq ID	Mögliche Deletionen (Δ) (AS-Position/AS-Anzahl)	Einfügestellen (Ω) von den Inserts		(AS-Position/Seq ID)
			Brückenbnd. 1,2,3 (Seq ID 1-3)	native Brückenbnd. 1 (Seq ID 4)	
gag (500 AS)	I.	Δ 1/131	Ω 132(1/3)	Ω 249(4)	
		Δ 159/150	Ω 249(2/3)	Ω 323(4)	
		Δ 363/14	Ω 323(1/2/3)	Ω 450(4)	
		Δ 450/50	Ω 450(1/2/3)		
pol 1 (561 AS)	II.	Δ 1/60	Ω 61(1/2/3)	Ω 61(4)	
		Δ 398/29	Ω 228(1/2/3)	Ω 284(4)	
		Δ 441/120	Ω 284(1/2/3)	Ω 436(4)	
			Ω 535(1/2/3)	Ω 535(4)	
pol 2 (289 AS)	III.	Δ 100/40	Ω 31(1/2)	Ω 140(4)	
		Δ 163/14	Ω 100(1/2/3)	Ω 177(4)	
			Ω 140(2/3)		
			Ω 177(1/3)		
env 1 (491 AS)	IV.	Δ 1/4	Ω 44(1/2/3)	Ω 87(4)	Ω 3(14/17/29-36)
		Δ 54/18	Ω 87(1/2/3)	Ω 136(13-36)	Ω 75(13-20/24/27/31)
		Δ 136/1	Ω 160(1/2/3)	Ω 160(4)	Ω 137(13-25/35)
		Δ 230/20	Ω 253(1/2/3)	Ω 253(4)	Ω 213(13-18/23-36)
		Δ 489/2	Ω 417(1/2/3)		Ω 392(13-36)
					Ω 452(19/21/34)
env 2 (392 AS)	V.	Δ 1/46	Ω 8(1/2)		Ω 8(5-8/9/11/12)
		Δ 142/13	Ω 112(1/2/3)		Ω 45(9-11)
		Δ 210/5	Ω 215(1/2/3)		Ω 161(5/7/8)
		Δ 240/23	Ω 344(1/3)		Ω 202(6/7)
env 3 (360 AS)	VI.	Δ 2/38	Ω 69(1/2/3)		Ω 214(6-8)
		Δ 257/103	Ω 176(1/2/3)		Ω 215(9-12)
			Ω 253(1/2/3)		Ω 286(10/11)
					Ω 344(9-12)

2. Aminosäuresequenzen (Single Letter Aminosäurecode) der Insertionen

Seq ID	Aminosäuresequenz	Seq ID	Aminosäuresequenz
1	GKR--K-RK--RRG	20	IRQIHIGPGRFAAW
2	G-KK-RR-KGK-RR-KK-G	21	DVQEMRIGPMAWSMG
3	G-C-K-R-KRRXRR-K--C-G	22	ICTRRGIRMGPGQVVYATCT
4	GVA--K-KRR---REKRAVG	23	TIVQIKIIGPLAVYSMYG
5	WQLQQRNLNLWGCRGKLICYTN	24	TRKSVRIGPGQAFYAT
6	WIONQQLNLWGCKGRILVCYTN	25	GHTRKSIRIGPGQTFYAT
7	WLQNOQLNLWGCKGRILICYTN	26	NTRQSTHIGPGALYTTKIE
8	WLQSQQLLSNWGCRGKLVCYTN	27	TRKSIHLPGQAFYATGD
9	AIERYLQDQARLNSWGCTFRQVCH	28	YQTRKSIRIGPGQAFYATGD
10	AMEKYLKDQAIIVNSWGCAFRQVCY	29	TVQEIIRIGPMAWYSMGNV
11	AMEKYLKDQARLNSWGCAFRQVCH	30	TRISHTIGPGRVFYRT
12	AI EKYLKHAQLN AWGCAFRQVCH	31	TRKGIHMGPGQVLYATKP
13	TRKSIHIGPGQAFYATGD	32	HTRKSIHIGPGRAFYATS
14	TRRSISFGIGPGQALYTT	33	TRKSIHIGPGRAFYTTSMQ
15	TRQRTPIGLQALYTTGQF	34	QTRTSITIGPGQVFYRTE
16	RTVQEIIRIGPMAWYSMGA	35	GTRKSVRIGPGQTFYATG
17	TMKRTSIHIGPGQTFYAT	36	TRKGIHIGPGRAFYATG
18	TRRGIPLPGRAWYATL	37	AVGIGINCTRPNNN
19	DSTRESMRIGPGQAFYATG	38	GDIIGDIRQAHCNIGPTPT

Legende: X ≡ D oder E
 "-" ≡ beliebige Aminosäure

Patentanhang

Fig. 1

1. Aminosäuresequenzen (Single Letter Aminosäurecode)

Seq ID I.: gag (500 AS)

M¹GARSVLGGELDRWEKIRLRPGGKKYK¹KLHIVASRELERFAVNPGLLETSEGRQILQQLPSLQTSSEELRSLYNTVATLYCVHQRIEIKDTK
EALDKIEEQKSKKKAQAAADTGHNSQVSN¹Y¹1/3¹PIVQNIQGMVHQAI¹SPRTLNAWVKV¹EEKAFSP¹PEVI¹PMFSALSEGATPQDLNMTL
NTVGGHQAAMQMLKETINEEAAEWDVRVPHAGPIAPGOMREPRGSDIAGTSTLQEQIGW¹2/3¹MTNNPPIPVGEIYKRWIILGLN¹KIVRMVSPTSI
LDIRQGPKEPRDYVDRFYKTLRAEQ¹2/3¹QVKNWMTETLLV¹1/2¹3¹QANANPDKCTILKALGPAATLEEMTACQGVGGPGHKARVL¹AEAMSV
TNSATIM¹QMRGNFRNQKIVKFCNGCKEGHTARNCRAPRKKGCKGCKGEGHQM¹KDCTERQANFLGKIWP¹SYKGRPGNFLO¹1/2¹3¹SRPEPTAP
PEESFRSGVETTPPQKQEPIDKELYPLTSLRSLFGNDPSSQ¹

Seq ID II.: pol 1 (561 AS)

M¹PISPIETVPVVKLPGM¹DPKVKOMPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPV¹1/2¹3¹FALKKKDSTKWRKLVDFRELNKRQTQDFW
EVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP¹SINNETPGIRYQYNVL¹PQGWKGS¹PAIFQSSMTKILEPFRKQNPNI¹VIYQYMDDL
YVGSLEIGQHRTKTEELRQHLRLWGLTTPDKKHQKEPPF¹1/2¹3¹LWMGYELHPDKWTVQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGIKVRQL
CKLI¹1/2¹3¹RGTKALTEVIPLEEAELEAENREILKEPVHGVYDPSKDLIAEIQKQGOWTYQIYQEPFN¹LKTGKYARMGAHTNDVKQLTE
AVQKITTESIV¹WGKTPKFKLPIQKET¹EWETWTEYQATWIPEWEFVNTPLVKLW¹YQLEKEPIV¹1/2¹3¹GAETFYVDGAANRET¹KLKGAGYVT
NRGRQKVVTLTDTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNIIEQLIKKEKVYLA¹1/2¹3¹WVPAHKGIGGNEQV¹DKL
VSAGIRKVL¹

Seq ID III.: pol 2 (289 AS)

MFLDGIDKAQDEHEKYHNSWRAMASDENLPP¹1/2¹3¹VVAKEIVASCDKCOLKGEAMHGQVDCSPGIWQLDCTHLEGKVLVAVHVASGYIEAEVIPA
ETGQETAY¹1/2¹3¹FLLLKLAGRPVKTIHTDNGSNFTSATVKAACWAGIKQEPF¹1/2¹3¹GIPYNPQSQGVVESMKNELKKI¹1/2¹3¹GQVRDQAEH
LKTAV¹1/2¹3¹QMAVFTHNFKRKGIGGYSAGERIVDIATDIQTKELQKQITKIQNFVYRDSRNPLWKGP¹AKLLWKGEGAVVIQD¹NSDIKVVPR
RKAKIIRDYGKQWAGDDCVCASRQDED

Seq ID IV.: env 1 (491 AS)

M¹DG¹14/17/29-36¹SH¹G¹TEKLVTVYGVVWKEAT¹TLFCASDAKAY¹12/31¹WATHACVPTD¹PNPQEVLVNVTFENFMW¹
¹KND413-20/24/27/31¹WVEQMHEIISL41/2/31¹WDQSLKPCVKLTPLCVSLKE¹CTDLKNDTNTNSSGRMIMERGEIKNCS¹FF13-36¹PP¹
¹13-25/35¹NISTSRGKVQKEYAFFYKLDII¹11/2/31¹PIDNDTTSYKLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNKTFNGT413-18¹
¹23-36¹GPTCNVSTVQCHGIR¹PPVSTQLLNGSLAE¹EVVIRSV411/2/31¹INFNDNAKTIIVQLNTSVEINCTRPNNNTRKRIRIQRGPRAFVT¹
¹IGKIGNMRQAH¹CNISRAKNWNTLKQIASKLREOFGNKTIIFKQSSGGDEIVTHSFNCGEFFYCNSQTFNSTWFNSTWSTEGSNTEGSD¹LO¹
¹3-36¹TTITLPCR¹IKIINNWKVGKAMYAP¹11/2/31¹PISGOIRCSSNITGLLLTRDGGNSNNESEIFRPGG419/21/31¹GDMRDNRSELYKYKV¹
¹KIEPLGVAPTAKRRVVQRE¹KR¹

Seq ID V.: env 2 (392 AS)

M¹GSDMRDN41/2/5-8/9/11/12¹WRSELYKYKVVKIEPLGVAPTAKRRVVQREKRAVGIGS419-11¹ALFLGLGAAGSTMGAASMTLTVOA¹
¹ROLLSGIVQOQNLLRAIEAQHLLQLTWVGIKQLOARIL411/2/31¹FAVERYLKQQLIGWCGSKLICITAVPWN¹ASWSNKSLEQIWN¹N¹WTWME¹
¹15/17/84¹WDREINNYTSLIHSLTEESQOQKEQEELLELDKWSLWN416/17/2/3/9/12¹WYIKLFIMIVGG¹
¹LVGLRIVFAVLST41VNRVRQGYSPLSFQTHLPIPRGP¹DRPEGIEEGGERDRDRSIRLVN4110/11¹GSLALIWDLLRSICLFSYHRLRDLILLIVT¹
¹RIVELGLRRGWEALKYWNLLQYWSQELK411/3/9-12¹NSAVSLNATAIAVAEGTDRVIEVVQACRAIRHIPRIRQGLERILL¹

Seq ID VI.: env 3 (360 AS)

MM¹SSAHGRHTRGVFVLGFLGLTAGSAMGAASLTVSQAQ¹RTLLAGIVQOQQLLDVVKRQOELLRLTV411/2/31¹WGTKNLQARVTAIEKYLQDOA¹
¹RLNSWGCFAFRQVCHTVPVWNDSLAPDWNMTWQEWKQVRYLEANISKSLEQAIQQEKNMYELQKLSWDIFGNWFDLTSWVKNT412/31¹YIQVG¹
¹VLIIVAVIALRIVIVYQMLSRRLKGYRPVFSSPGYIQOIHIHDKRGQ¹SPANETEEDGGSGGDRYPWP4117/2/31¹IAYIT¹HFELIROLIRLLTRL¹
¹YSICRDLRSRFTLQLIYQNLRDWLRRLRTAFLQYGCWEIQEAFQAAARATRETLAGACRGLWRVLERIGRILAVPRRIRQGAIEALL¹

Legende: ¹ bzw. ¹ ≡ Anfang bzw. Ende einer möglichen Deletion

¹AB¹ ≡ Mögliche Einfügestellen (Insertionsstellen) einer AS-Sequenz mit der Seq ID A und/oder B

4. Beispielproteine aus der Permutationstabelle (A, B und C) und andere (D und E)

A. pol 2 Δ 100/40, 140/23, 163/14 Ω 31/2, 100/3 (253 AS)

MFLDGIDKAQDEHEKYHSNWRAMASDFNLPPGPKARRIKGKMRVRKAGVVAKEIVASCDKQLKGEAMHQVDCSPGIWQLDCTHLEGGKVLIVAVHV
ASGYIEAEVIPAETGQETAYGACIKHRYKRRDRKHKVACTGQMAVFTHNFKRKGIGGSAGERIVDIITATDIQTKELOKITKIQNFVRVYYRDSRNP
LWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGGQWAGDDCVASRQDED

B. env 2 Δ 47/25, 210/5, 215/25, 240/23, 286/58, 344/48 Ω 215/11 (232 AS)

MGSDMRDNWRSELYKYKVVKTIEPLGVAPTKAKRRVVQREKRAVGIGSRQLLSGIVQQNNLLRAIEAQQHLLIQLTVWGIKQLQARILAVERYLKDQQLL
GIWCSGKLICTTAVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSIEESQNOQEKNEQELLELDKWASLWNNWFNITNLWAMEKYLKQDQARLN
SWGCAFRQVCHDRPEGIEEGGERDRDRSIRLVN

C. env 2 Δ 47/25, 210/5, 215/25, 240/23, 286/58, 344/48 Ω 8/6, 215/11 (254 AS)

MGSDMRDNWIQNNQOLLNLWGCKGRLLVCYTNWRSELYKYKVVKTIEPLGVAPTKAKRRVVQREKRAVGIGSRQLLSGIVQQNNLLRAIEAQQHLLIQLTVW
GIKQLQARILAVERYLKDQQLLGIWCSGKLICTTAVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSIEESQNOQEKNEQELLELDKWASLW
NWFNITNLWAMEKYLKQDQARLNSWGCAFRQVCHDRPEGIEEGGERDRDRSIRLVN

D. AS (M) + Seq ID (1+37+24+38+2+37+32+38+3+37+27+38+2+37+25+38+1) (297 AS)

MKRAHKSRIKRVTRRGAVGIGINCINTRPNNTRKSVRIGPGQAFYATGDIIGDIRQAHNCNIGPTPTGWKKNRRLKGYRRMKKWGAVGIGINCINTRPNN
NHTRKSIHIGPGAFYATSGDIIGDIRQAHNCNIGPTPTGACVKHRQKRKEKRYKTACVGAVGIGINCINTRPNNTRKSIHILGPGQAFYATGDDIIGDI
RQAHNCNIGPTPTGSKKARRIKGKMRRLKKVGAVGIGINCINTRPNNNGHTRKSRIGPGQTFYATGDIIGDIRQAHNCNIGPTPTGKRAVKSRYKRIHRRG













E. env 4 (221 AS)

MGSDMRDNWRSELYKYKVVKTIEPLGVAPTKAKRRVVQREALETLLQNNQOLLNLWGCKGRLLCYWGIIKQLQARILAVERYLKDQQLLGIWCSGKLICTT
AVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSIEESQNOQEKNEQELLELDKWASLWNNWFNITNLWAMEKYLKQDQARLNSWGCAFRQVCHDR
PEGIEEGGERDRDRSIRLVNGS

2

B
 E Q
 A V
 E I
 WC HD
 R
 NS
 QARL
 YLRD
 AMEK
 TNWL
 MFNI
 LWNW
 ASWS
 WASN
 ELDK
 EOELL
 SONOEOEN
 RORDRS IRLVNGS
 K
 G L
 S I
 E I
 LMG T
 LLG
 DOQ
 YLK
 VER
 ILA
 QHL
 AO LQ
 IE LT
 RA VM
 LL GI
 AV IV
 GS LL
 GI SG
 AV IV
 RQ
 G
 L V
 P A
 E P
 N
 W
 WIO
 GS
 DM
 M

→ 4.D.: AS(M) + Seq ID (1+37+24+38+2+37+32+38+3+37+27+38+2+37+25+38+1)


<-	Epitop	->	<-	Epitop	->						
<table border="0"> <tr> <td colspan="3"> GPGCA RI FYA KSV TGD TR IIG NN DI PN RO TR AH  </td> <td colspan="3"> PGRAFV HIG ATG KSI GD TR IIG NNH DI PN RO TR AH  </td> </tr> </table>						GPGCA RI FYA KSV TGD TR IIG NN DI PN RO TR AH 			PGRAFV HIG ATG KSI GD TR IIG NNH DI PN RO TR AH 		
GPGCA RI FYA KSV TGD TR IIG NN DI PN RO TR AH 			PGRAFV HIG ATG KSI GD TR IIG NNH DI PN RO TR AH 								
<table border="0"> <tr> <td colspan="3"> AVGIN NIGPPT GKRAHKSRKTRVTHRG <--- pos. Brücke --> </td> <td colspan="3"> AVGIN NIGPPT GSKKURALCKYRRMKWG <--- pos. Brücke --> </td> </tr> </table>						AVGIN NIGPPT GKRAHKSRKTRVTHRG <--- pos. Brücke -->			AVGIN NIGPPT GSKKURALCKYRRMKWG <--- pos. Brücke -->		
AVGIN NIGPPT GKRAHKSRKTRVTHRG <--- pos. Brücke -->			AVGIN NIGPPT GSKKURALCKYRRMKWG <--- pos. Brücke -->								
<table border="0"> <tr> <td colspan="3"> GPGQAFYA IHL TGD KS GD TR IIG NN DI PN RO TR AH  </td> <td colspan="3"> GPGQTFY IRI AT RKS GD GHT IIG NN DI PN RO TR AH  </td> </tr> </table>						GPGQAFYA IHL TGD KS GD TR IIG NN DI PN RO TR AH 			GPGQTFY IRI AT RKS GD GHT IIG NN DI PN RO TR AH 		
GPGQAFYA IHL TGD KS GD TR IIG NN DI PN RO TR AH 			GPGQTFY IRI AT RKS GD GHT IIG NN DI PN RO TR AH 								
<table border="0"> <tr> <td colspan="3"> AVGIN NIGPPT GACVHROKQKRRKVKACVG <--- pos. Brücke --> </td> <td colspan="3"> AVGIN NIGPPT GSKKARRIKGMRRLKVG <--- pos. Brücke --> </td> </tr> </table>						AVGIN NIGPPT GACVHROKQKRRKVKACVG <--- pos. Brücke -->			AVGIN NIGPPT GSKKARRIKGMRRLKVG <--- pos. Brücke -->		
AVGIN NIGPPT GACVHROKQKRRKVKACVG <--- pos. Brücke -->			AVGIN NIGPPT GSKKARRIKGMRRLKVG <--- pos. Brücke -->								

INTROZELLULOSE MEMBRAN

B. Negatives Beispiel (4.E.): env 4

ILAV
 AR ER
 LQ YLK
 KQ DOOL
 GI LGI
 YW WG
 LI SG
 R₁ LI
 KG LI
 LMG T
 ILN T
 NOQ A
 LLQ V
 LET P
 FA W
 G
 L V
 P A
 E P
 GS
 NM
 RDNWSELYKKVVKI TRAKRNVOR
 NASNSKSLEQIWNMT
 Y
 NN TS
 EI LI
 DR HS
 EN LI
 WM PE
 SONOFEKN
 NITROZETULULOSLMEBRAN

R
 F Q
 A V
 WG HD
 NS R
 P
 QARL
 YLKD
 ALEX
 TNWL
 WFNI
 LANN
 ASWS
 WASN
 ELDK
 FOELL
 E
 G
 E
 E
 I
 G
 E
 RDRDRSIRLVNGS

- Legend:
- Aminosäure in rot ≡ positiv geladene Aminosäure
 - Aminosäure in blau ≡ negativ geladene Aminosäure
 - Aminosäure in grün ≡ polare Aminosäure
 -  ≡ Brückenbindung von zwei Cysteinen